#4

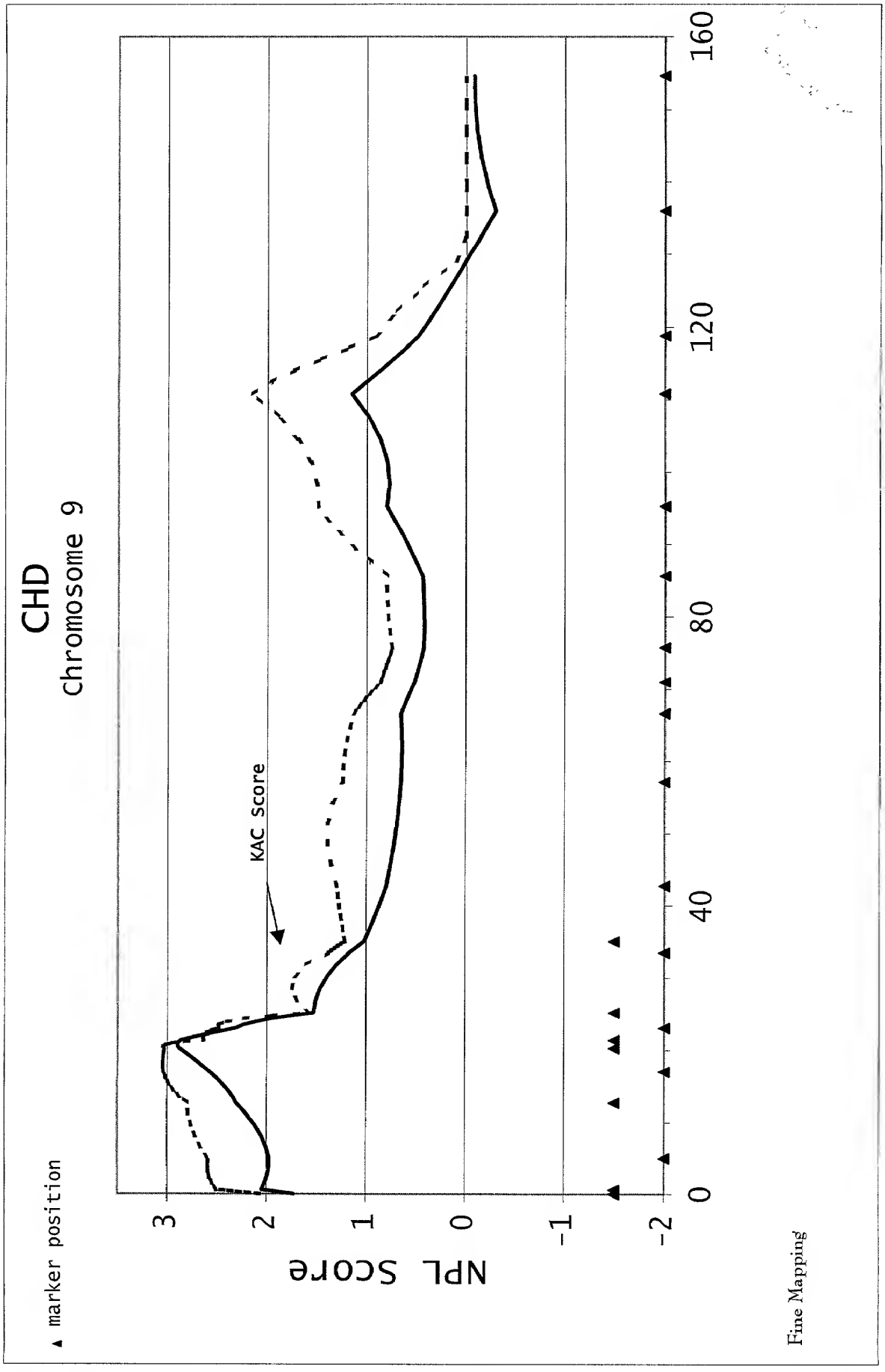
CHD
Chromosome 9
NPL Score
3
2
1
0
-1
-2
0
40
80
120
160
KAC Score
marker position
Fine Mapping

Fig. 1

BREAKDOWN BY SUBJECT (using individuals with complete genotypes)

# of subjects containing at least one of the following VLDLr alleles

frequency (column percentage)

VLDLr	Cases (N=204)			Controls (N=117)			Odds Ratio (*p-value*)		
allele#	Males (N=148)	Females (N=56)	Total	Males (N=75)	Females (N=42)	Total	Males	Females	Total
5	91 (59.5)	35 (60.3)	126 (59.7)	55 (71.4)	28 (66.7)	83 (69.7)	0.59 (0.083)	0.78 (0.57)	0.64 (0.079)
7	0 (0.0)	1 (1.7)	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	0.50 (1.00)	2.22 (1.00)	1.70 (1.00)
8	74 (48.4)	27 (46.6)	101 (47.9)	31 (40.3)	23 (54.8)	54 (45.4)	1.39 (0.24)	0.72 (0.55)	1.11 (0.73)
9	80 (52.3)	29 (50.0)	109 (51.7)	36 (46.8)	15 (35.7)	51 (42.9)	1.25 (0.46)	1.80 (0.22)	1.42 (0.14)
10	2 (1.3)	0 (0.0)	2 (0.9)	0 (0.0)	1 (2.4)	1 (0.6)	2.58 (1.00)	0.24 (0.42)	1.13 (1.00)
11	1 (0.7)	1 (1.7)	2 (0.9)	1 (1.3)	0 (0.0)	1 (0.8)	0.50 (1.00)	2.22 (1.00)	1.13 (1.00)

Fig. 2A

BREAKDOWN BY ALLELE (includes partial genotypes)

frequency (column percentage)

VLDLr allele#	Cases (N=415)			Controls (N=236)		
	Males (N=301)	Females (N=114)	Total	Males (N=152)	Females (N=84)	Total
5	112 (37.2)	43 (37.7)	155 (37.3)	73 (48.0)	37 (44.0)	110 (46.6)
7	0 (0.0)	1 (0.9)	1 (0.2)	0 (0.0)	0 (0.0)	0 (0.0)
8	89 (29.6)	36 (31.6)	125 (30.1)	36 (23.7)	27 (32.1)	63 (26.7)
9	97 (32.2)	33 (28.9)	130 (31.3)	42 (27.6)	19 (22.6)	61 (25.8)
10	2 (0.7)	0 (0.0)	2 (0.5)	0 (0.0)	1 (1.2)	1 (0.4)
11	1 (0.3)	1 (0.9)	2 (0.5)	1 (0.7)	0 (0.0)	1 (0.4)

Males (p-value- CLUMP 10000 sims): **0.19**

Females (p-value- CLUMP 10000 sims): **0.62**

Total (p-value- CLUMP 10000 sims): **0.33**

Fig. 2B

BREAKDOWN BY GENOTYPE

frequency (column percentage)

VLDLr genotype	Cases (N=204)			Controls (N=117)			Odds Ratio (*p-value*)		
	Males (N=148)	Females (N=56)	Total	Males (N=75)	Females (N=42)	Total	Males	Females	Total
5/5	21 (14.2)	8 (14.3)	29 (14.2)	18 (24.0)	9 (21.4)	27 (23.1)	0.52 (0.089)	0.61 (0.42)	0.55 (0.044)
5/7	0 (0.0)	1 (1.8)	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	0.51 (1.00)	2.30 (1.00)	1.73 (1.00)
5/8	33 (22.3)	10 (17.9)	43 (21.1)	16 (21.3)	13 (31.0)	29 (24.8)	1.06 (1.00)	0.48 (0.15)	0.81 (0.48)
5/9	35 (23.6)	15 (26.8)	50 (24.5)	21 (28.0)	6 (14.3)	27 (23.1)	0.80 (0.52)	2.20 (0.21)	1.08 (0.78)
5/10	2 (1.4)	0 (0.0)	2 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)	2.58 (0.58)	0.75 (1.00)	2.90 (0.54)
5/11	0 (0.0)	1 (1.8)	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	0.51 (1.00)	2.30 (1.00)	1.73 (1.00)
8/8	15 (10.1)	7 (12.5)	22 (10.8)	5 (6.7)	4 (9.5)	9 (7.7)	1.58 (0.47)	1.36 (0.76)	1.45 (0.44)
8/9	24 (16.2)	10 (17.9)	34 (16.7)	8 (10.7)	5 (11.9)	13 (11.1)	1.62 (0.31)	1.61 (0.57)	1.60 (0.19)
8/10	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (2.4)	1 (0.9)	0.51 (1.00)	0.24 (0.47)	0.19 (0.36)
8/11	1 (0.7)	0 (0.0)	1 (0.5)	1 (1.3)	0 (0.0)	1 (0.9)	0.50 (1.00)	0.75 (1.00)	0.57 (1.00)
9/9	17 (11.5)	4 (7.1)	21 (10.3)	6 (8.0)	4 (9.5)	10 (8.5)	1.49 (0.48)	0.73 (0.72)	1.23 (0.70)

Males (p-value- CLUMP 10000 sims): **0.47**

Females (p-value- CLUMP 10000 sims): **0.44**

Total (p-value- CLUMP 10000 sims): **0.38**

Fig. 2C

BREAKDOWN BY GENOTYPE (collapsing groups)

frequency (column percentage)

VLDLr genotype	Cases (N=204)			Controls (N=117)			Odds Ratio (*p-value*)		
	Males (N=148)	Females (N=56)	Total	Males (N=75)	Females (N=42)	Total	Males	Females	Total
5/5	21 (14.2)	8 (14.3)	29 (14.2)	18 (24.0)	9 (21.4)	27 (23.1)	0.52 (0.049)	0.61 (0.42)	0.55 (0.044)
5/not 5	70 (47.3)	27 (48.2)	97 (47.5)	37 (49.3)	19 (45.2)	56 (47.9)	0.92 (0.77)	1.13 (0.65)	0.99 (1.000)
not 5/not 5	57 (38.5)	21 (37.5)	78 (38.2)	20 (26.7)	14 (33.3)	34 (29.1)	1.72 (0.10)	1.20 (0.83)	1.51 (0.110)

Males (p-value- CLUMP 10000 sims): **0.091**

Females (p-value- CLUMP 10000 sims): **0.280**

Total (p-value- CLUMP 10000 sims): **0.075**

Fig. 2D

	VLDLR														
		TDT					**S-TDT**					**Combined Scores**		
	Allele	b	c	Chi-Sq		Y	Mean(A)	Var(V)	z'		W	Mean(A)	Var(V)	z'
	5	1	5	2.667		64	65.888	10.958	.419*		65	68.888	12.458	0.96
	8	5	1	2.667		55	48.3	13.043	1.717		60	51.3	14.543	2.15
	9	0	0	N/A		45	50.412	11.382	1.456*		45	50.412	11.382	1.456
	7	0	0	N/A		2	1.2	0.36	0.5		2	1.2	0.36	0.5
	allele	**p-values**												
	5	0.17												
	8	**0.016**												
	9	0.073												

Fig. 3